Supplementary Materials

Combined Drug-Resistance Mutations Substantially Enhance Enzyme Production in *Paenibacillus agaridevorans*

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Fig. S1. CITase production by cells grown with various carbon sources. Strains were grown for 72 h in LB-Dex medium containing 2% dextran 40 or LB medium containing 2% glucose, maltose, sucrose, isomaltooligosaccharides Fujioligo G67, dextrin, or soluble starch. CITase activity was measured as in Fig. 1 in the main text.
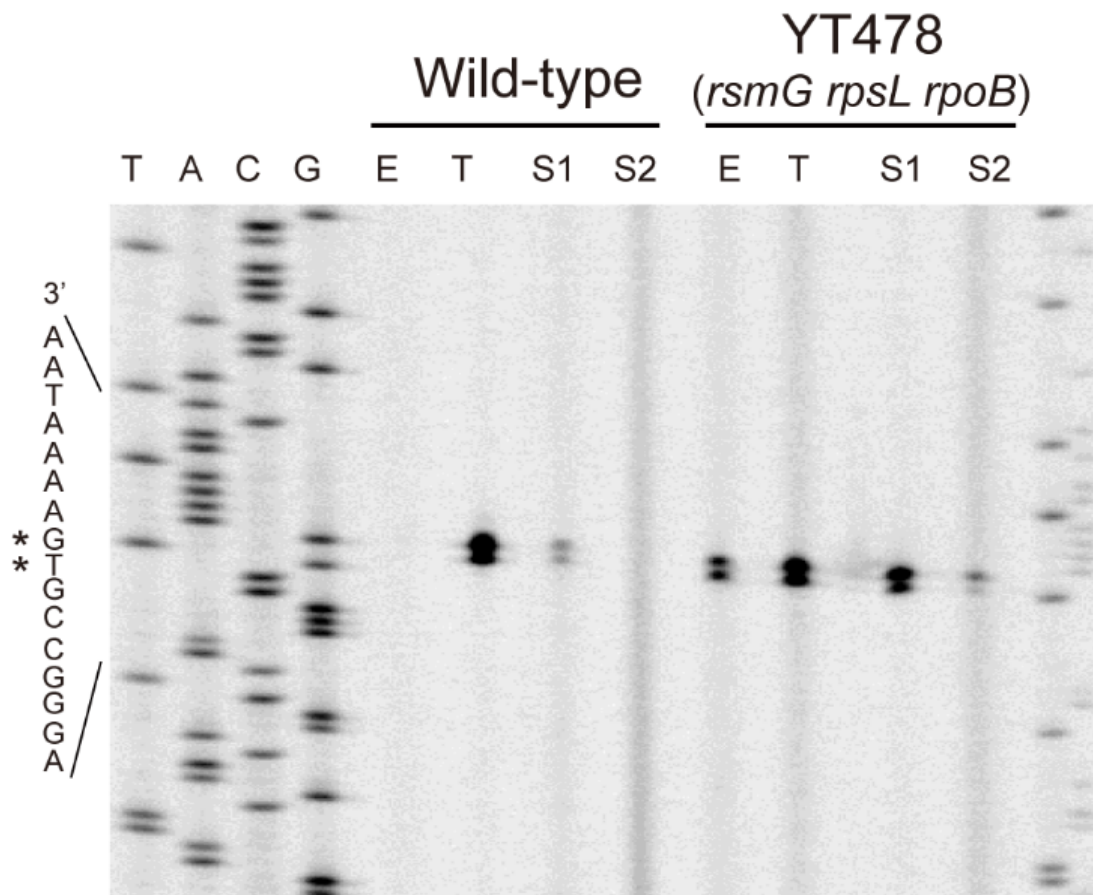
Fig. S2. Primer extension analysis of *cit*. Primer extension analysis was performed with 50 µg RNA and 1 pmol of an infrared dye-labeled primer for the CITase gene (*cit*), IRD800-CITase (5'-IRD800-GGAGGGGATACGACGGATGCGACG-3') (Aloka). Primer extension and sequencing reactions were run on polyacrylamide gels, followed by analysis using the DNA sequencing system LIC-4200L(S)-2 (LI-COR). E, T, S1, and S2 indicate exponential phase (OD600=0.2), transition phase (OD600=0.7), early stationary phase (12 h after transition phase) and late stationary phase (24 h after transition phase), respectively.
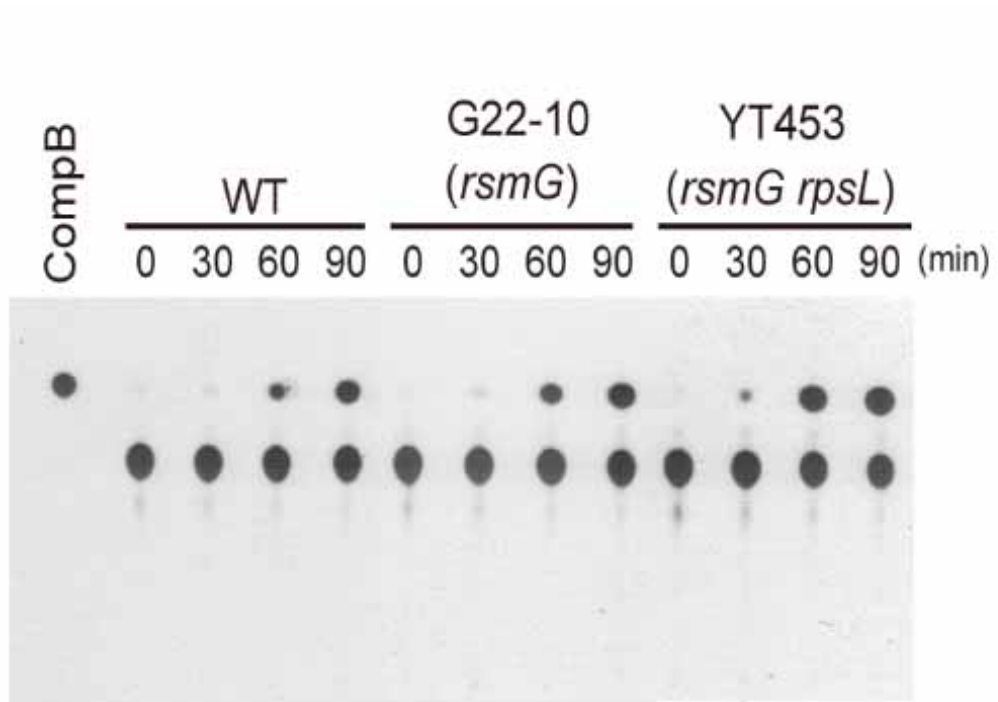
Fig. S3. In vitro protein synthesis activities of mutant strains as determined by chloramphenicol acetyltransferase (CAT) activity. Strains were grown to late exponential phase (OD_{600} 0.4), and cell-free synthesis of CAT by washed ribosomes was performed as described in the main text.
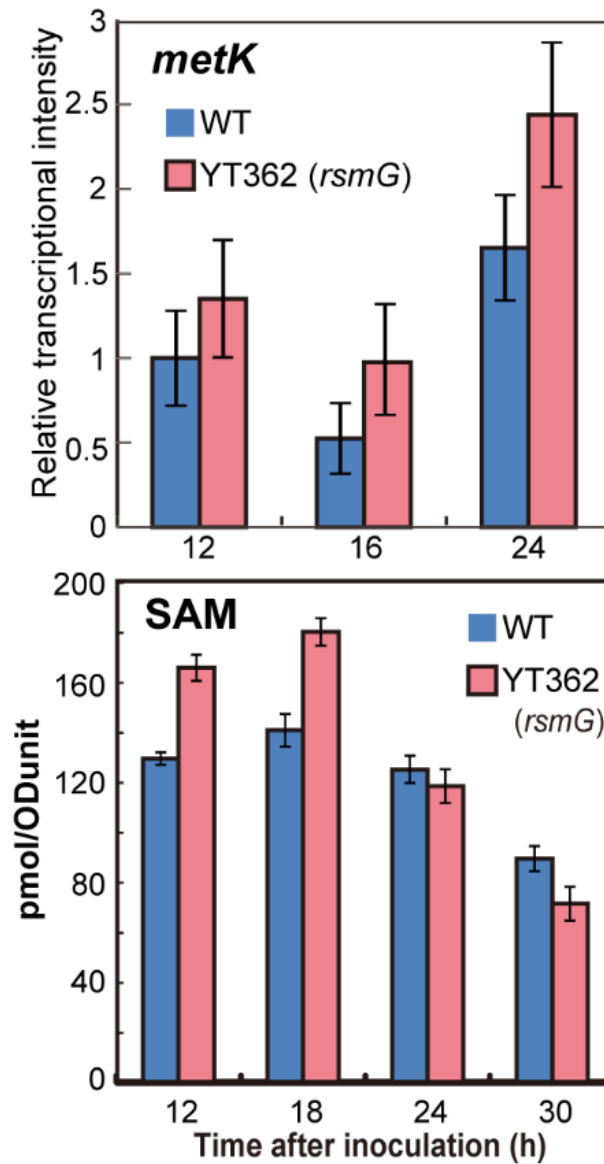
Fig. S4. Transcriptional analysis of the *metK* gene encoding *S*-adenosylmethionine (SAM) synthetase (upper) and intracellular SAM level (lower) in the wild-type and *rsmG* mutant YT362 strains. Strains were grown in LB-Dex medium for the indicated times. Transcription of *metK* and SAM pool size were determined as described in the main text.
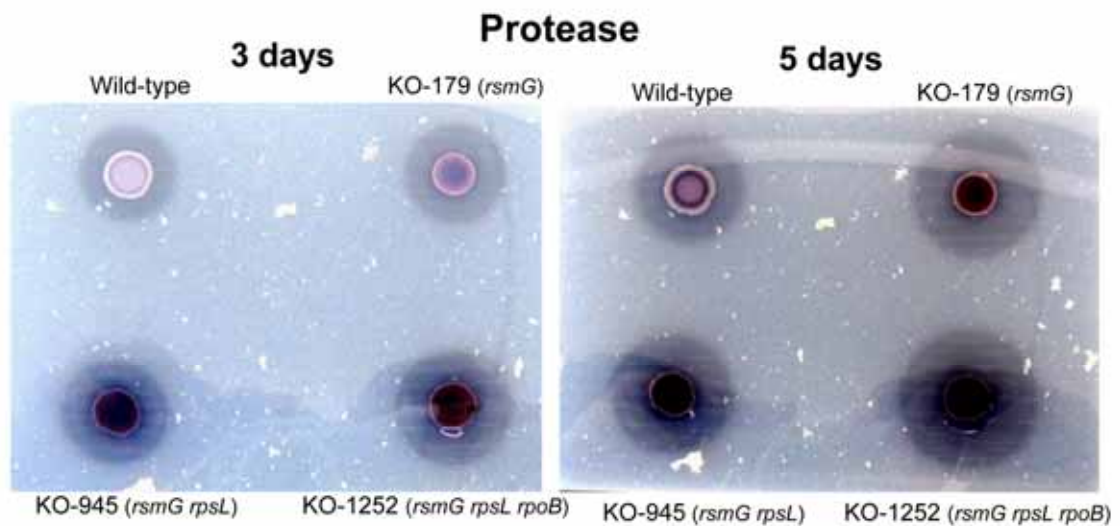
Fig. S5. Production of protease by *Streptomyces coelicolor* A3(2) and its mutant strains. Strains were grown at 30 ˚C for the indicated periods on skim-milk agar plate for protease production. The halo represents degradation of skim-milk by protease.
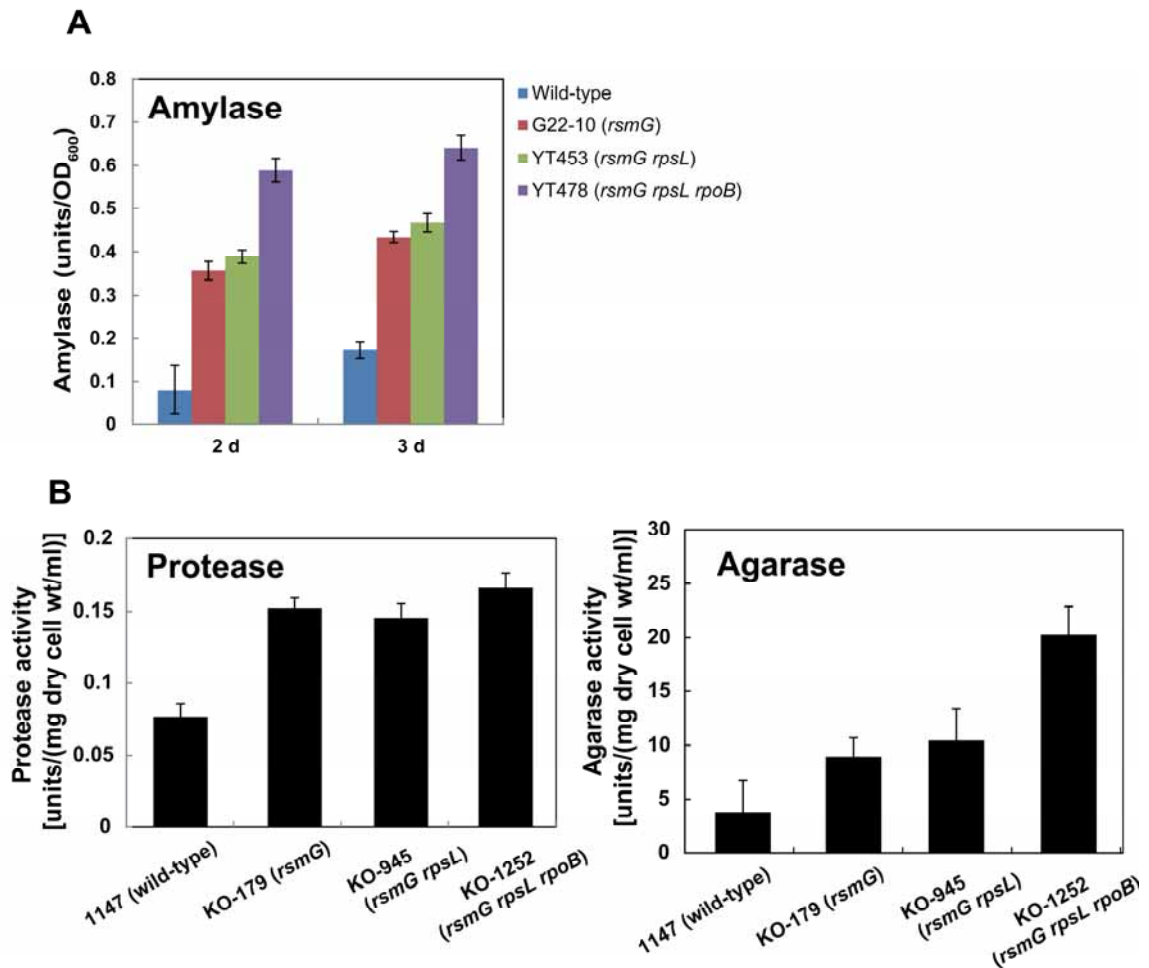
Fig. S6. Enzyme production by the wild-type and mutant strains of *P. agaridevorans* and *S. coelicolor*. (A) Production of amylase by the *P. agaridevorans* wild-type, single, double, and triple mutant strains. (B) Production of protease by *Streptomyces coelicolor* A3(2) and its mutant strains. Productivity of the enzymes are expressed as enzyme activity per unit cell amount (OD600 or mg dry cell weight).

Table S1.   Primers used in this study.

Application purpose	Primer name	Oligonucleotide sequence (5' 3')
PCR and sequencing of *rsmG*	rsmG-F	GGTGTTACGCCGGCAGACATTTC
	rsmG-R	GAAGTGCTATTCCCGCATGATAACGTAG
PCR and sequencing of *rpsL*	rpsL-F	GTTTCCGACATGTACGGGAATTGTCAATTC
	rpsL-R	GGCATGTAAAGTCCCCCTTTCTTCTAATAG
PCR and sequencing of *rpoB*	rpoB-F	GTBGTKCGTGARMGDATGTCNATYCAAGA
	rpoB-R	ACVGCYTGRCGYTGCATGTTYGCDCCCAT
Real-time PCR of the CITase gene	RT-CITase-F	CGGCAACTCCATTGATCTCTCCACAC
	RT-CITase-R	GCTTCGTAACGCGTGCCGGCATTGTC
Real-time PCR of 16S rRNA	RT-16S-F	GAATGCTAGGTGTTAGGGGTTTCGATAC
	RT-16S-R	CTAAGATCAAGGGTTGCGCTCGTTGC
Real-time PCR of *metK*	RT-metK-F	GGTCTAACGGGACGGAAAAT
	RT-metK-R	AGCTGCTGAACGATCAACCT

Table S2. Genes encoding carbohydrate-active enzymes (CAZymes) of _Paenibacillus agaridevolans_ T-3040

Locus tag	CAZy family (amino acid residues)
PAT3040_00009	AA7(22-245)
PAT3040_00021	GH88(36-362)
PAT3040_00036	GH38(240-511)
PAT3040_00040	CBM32(171-275),CBM32(335-442),CBM32(487-602),GH141(671-1057)
PAT3040_00041	GH106(4-703)
PAT3040_00053	CBM32(1201-1329)
PAT3040_00072	PL26
PAT3040_00074	GH63(65-365)
PAT3040_00077	CE10(14-255)
PAT3040_00078	GH105(381-724)
PAT3040_00098	GH129(321-587)
PAT3040_00104	CBM16(36-150),CBM9(321-476),CBM16(800-862),GH42(922-1215)
PAT3040_00105	GH36(7-498)
PAT3040_00106	GH39(101-352)
PAT3040_00107	CE10(34-256)
PAT3040_00113	GT83(9-204)
PAT3040_00115	CBM50(627-675)
PAT3040_00118	CBM67(10-204),GH78(269-781)
PAT3040_00125	GT2(60-260)
PAT3040_00127	GH5(88-415)
PAT3040_00137	GH39(773-994),CBM9(1297-1448)
PAT3040_00142	CBM16(43-150),CBM9(332-485),CBM16(747-864),GH42(922-1114)
PAT3040_00149	CE3(52-196)
PAT3040_00150	CBM66(77-231),CBM66(242-376),GH136(390-783),CBM9(1062-1262)
PAT3040_00154	GH109(4-118)
PAT3040_00163	CBM32(33-127),CBM6(188-294)
PAT3040_00166	GH2(17-497)
PAT3040_00167	GH43(46-309),CBM66(354-476),CBM66(682-837)
PAT3040_00173	CBM6(526-645),CBM6(655-779),CBM6(809-922)

PAT3040_00203	CBM44(465-514)
PAT3040_00213	GH38(7-262)
PAT3040_00214	GH63(234-596)
PAT3040_00215	CBM54(207-314)
PAT3040_00216	CBM67(81-238),GH78(279-783)
PAT3040_00223	GH28(18-366)
PAT3040_00227	CBM16(65-119),CBM16(192-274)
PAT3040_00234	GH99(29-366)
PAT3040_00236	CBM32(237-351),GH140(367-686),CBM32(789-894),CBM32(920-1027),CBM56(715-804)
PAT3040_00259	CBM50(35-79),CBM50(88-134),CBM50(142-189)
PAT3040_00278	CBM16(31-153),GH123(669-890)
PAT3040_00280	CBM67(12-127),GH78(276-772)
PAT3040_00281	GH36(113-607)
PAT3040_00287	GH2(2-735)
PAT3040_00298	PL1(406-587)
PAT3040_00317	CBM9(16-205)
PAT3040_00331	CBM44(187-260),CBM32(290-416),GH78(489-747),CBM32(943-1067),GH20(1297-1613),CBM32(1839-1962)
PAT3040_00338	GH78(165-646)
PAT3040_00339	GH20(87-402)
PAT3040_00356	GH106(14-693)
PAT3040_00357	GH15(294-497)
PAT3040_00358	GH109(4-119)
PAT3040_00359	GH109(3-100)
PAT3040_00363	GH129(83-482)
PAT3040_00367	CBM35(300-392)
PAT3040_00376	CBM9(1621-1796)
PAT3040_00379	GH78(161-645)
PAT3040_00381	CE15(19-340)
PAT3040_00407	GH88(42-366)
PAT3040_00459	GH4(3-179)
PAT3040_00460	CBM67(2-96),GH78(254-742)

PAT3040_00473	PL5(119-216)
PAT3040_00481	CBM66(199-320),CBM66(343-503),GH145(605-883)
PAT3040_00503	GH29(34-246)
PAT3040_00511	GH109(2-114)
PAT3040_00525	GH2(13-478)
PAT3040_00544	GH109(6-118)
PAT3040_00572	GT4(200-341)
PAT3040_00592	PL17(397-514)
PAT3040_00593	PL15(504-641)
PAT3040_00613	GH88(42-362)
PAT3040_00629	GH23(125-236)
PAT3040_00753	GT51(83-270)
PAT3040_00781	PL22(113-241)
PAT3040_00784	GH39(519-787),CBM9(1086-1232)
PAT3040_00791	GH109(5-120)
PAT3040_00804	GT2(5-103)
PAT3040_00885	GT2(5-119)
PAT3040_00889	GT2(5-127)
PAT3040_00890	GT2(1-150)
PAT3040_00891	GT4(194-349)
PAT3040_00892	GT2(8-141)
PAT3040_00896	GH109(5-114)
PAT3040_00923	CE14(11-120)
PAT3040_00930	GH4(9-185)
PAT3040_00938	CE4(316-437)
PAT3040_00959	CE1(91-231)
PAT3040_00970	GH123(84-528)
PAT3040_00972	GH109(3-57)
PAT3040_00976	PL9(140-431)
PAT3040_00987	CBM54(228-334),CBM9(1056-1203)
PAT3040_00988	GH29(23-192)

PAT3040_00989	GH2(25-557)
PAT3040_00994	GH109(15-132)
PAT3040_01001	CE4(25-142)
PAT3040_01007	GH18(251-549)
PAT3040_01009	GH109(2-116)
PAT3040_01010	GH109(66-113)
PAT3040_01017	GH33(27-352)
PAT3040_01018	GH117(44-122)
PAT3040_01019	CBM16(930-1052)
PAT3040_01020	CE3(19-204)
PAT3040_01039	GH51(3-502)
PAT3040_01099	GH38(4-271)
PAT3040_01113	CE9(3-375)
PAT3040_01183	CBM70(19-186),PL8(652-915)
PAT3040_01184	PL8(392-650)
PAT3040_01195	GT28(189-335)
PAT3040_01199	GH109(55-125)
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PAT3040_01221	GH2(36-905)
PAT3040_01282	CBM35(302-456)
PAT3040_01285	GH88(56-375)
PAT3040_01301	GT39(31-245)
PAT3040_01312	GT4(207-353)
PAT3040_01314	GT2(46-214)
PAT3040_01336	GH109(4-119)
PAT3040_01342	GH109(7-122)
PAT3040_01344	GH109(55-111)
PAT3040_01346	GH109(6-129)
PAT3040_01356	GH127(2-361)
PAT3040_01357	GH127(10-171)
PAT3040_01371	CBM53(9-64)

PAT3040_01387	CBM50(160-205)
PAT3040_01406	PL22(124-216)
PAT3040_01412	CE12(143-303)
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PAT3040_01418	GH109(3-103)
PAT3040_01419	GH109(47-118)
PAT3040_01420	GH109(8-110)
PAT3040_01429	GH109(4-118)
PAT3040_01430	GH28(216-563),CBM66(613-757),CBM66(886-1043)
PAT3040_01431	GH28(179-517),CBM66(551-708)
PAT3040_01440	CBM54(207-318),CBM22(609-739),CBM16(1375-1490),CBM22(1628-1744)
PAT3040_01457	CBM54(63-175),CBM16(1264-1367)
PAT3040_01463	GH2(10-569)
PAT3040_01486	GH4(3-175)
PAT3040_01487	GH109(4-118)
PAT3040_01493	CBM32(39-150),GH42(222-407),CBM38(965-1091),CBM38(1110-1248),CBM38(1267-1392),CBM32(1411-1474),CBM32(1484-1613)
PAT3040_01499	CBM32(4-125),GH42(207-400),CBM38(979-1112)
PAT3040_01501	GH29(7-329)
PAT3040_01503	GH2(139-749)
PAT3040_01504	GH95(247-702)
PAT3040_01505	CBM67(97-292),GH78(366-932)
PAT3040_01506	GH105(28-369)
PAT3040_01507	GH143(8-559)
PAT3040_01509	GH28(3-331)
PAT3040_01510	GH138(3-903)
PAT3040_01511	PL2(14-499)
PAT3040_01519	GH142(208-701
PAT3040_01520	GH33(37-340)
PAT3040_01522	GH140(102-369)
PAT3040_01524	CBM35(325-415)
PAT3040_01528	GH129(150-740)

PAT3040_01535	CE8(4-294)
PAT3040_01536	GH33(13-311)
PAT3040_01537	CE7(141-243)
PAT3040_01538	GH138(2-887)
PAT3040_01539	GH106(7-713)
PAT3040_01543	GH109(5-118)
PAT3040_01545	GH59(321-1049)
PAT3040_01551	CBM66(36-186),GH43(680-884),CBM57(1077-1160)
PAT3040_01553	GH88(43-366)
PAT3040_01569	PL8(407-665)
PAT3040_01571	GH88(59-386)
PAT3040_01573	CE13(36-220)
PAT3040_01590	CBM22(43-167),CBM22(205-317)
PAT3040_01640	CBM37(130-180),CBM37(220-262)
PAT3040_01663	GH105(44-356)
PAT3040_01670	CBM13(985-1113)
PAT3040_01704	CBM9(1159-1296)
PAT3040_01711	GH109(7-116)
PAT3040_01712	GH109(6-123)
PAT3040_01713	GH116(399-745)
PAT3040_01714	CBM6(10-109)
PAT3040_01715	CBM67(2-125),GH78(186-685)
PAT3040_01749	GT2(6-104)
PAT3040_01797	GH130(16-330)
PAT3040_01805	CBM13(17-145)
PAT3040_01811	CE14(4-111)
PAT3040_01815	GH95(1-729)
PAT3040_01823	GH101(48-524)
PAT3040_01824	GH109(1-119)
PAT3040_01849	GH78(163-629)
PAT3040_01870	GH109(1-109)

PAT3040_01880	CE3(19-204)
PAT3040_01883	CBM32(86-176),GH33(313-602)
PAT3040_01890	CE7(44-166)
PAT3040_01895	GH127(64-509)
PAT3040_01896	CBM32(31-151),CBM32(636-753),CBM32(871-991)
PAT3040_01897	GH99(50-351)
PAT3040_01917	CBM32(67-193),CBM32(688-807)
PAT3040_01934	CE4(15-136)
PAT3040_01935	CBM54(123-235),GH82(874-933)
PAT3040_01936	CBM6(681-776)
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PAT3040_02056	GH120(114-170)
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PAT3040_02067	GH110(17-567)
PAT3040_02077	GH36(166-407)
PAT3040_02078	GH129(10-631)
PAT3040_02080	GH5(12-394)
PAT3040_02081	GT32(61-132)
PAT3040_02082	GH29(4-315)
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PAT3040_02121	GH109(6-108)
PAT3040_02127	CBM40(164-241),GH136(253-734),CBM9(774-937)
PAT3040_02128	GH29(5-305),CBM32(321-392)
PAT3040_02172	GT103(34-105)
PAT3040_02186	CBM16(1124-1246)
PAT3040_02205	GH43(60-346),CBM35(373-495)
PAT3040_02208	GH105(48-370)
PAT3040_02215	GH109(34-97)
PAT3040_02217	PL1(253-440),CBM37(665-717)

PAT3040_02223	GT101(1-115)
PAT3040_02225	GT2(5-106)
PAT3040_02226	GH105(6-182)
PAT3040_02227	GT4(229-373)
PAT3040_02228	GT4(226-373)
PAT3040_02230	GT2(6-116)
PAT3040_02231	GT4(135-282)
PAT3040_02240	CBM32(882-1013),CBM40(334-445)
PAT3040_02245	CBM67(118-295),GH78(324-840)
PAT3040_02251	CE7(4-316)
PAT3040_02252	CBM40(1115-1193),CBM40(1295-1403)
PAT3040_02295	CBM16(918-1034)
PAT3040_02301	GH23(54-184)
PAT3040_02316	CBM32(39-164),GH20(391-697),CBM32(919-1039)
PAT3040_02317	CBM32(35-171),CBM32(713-834)
PAT3040_02324	GT51(72-247)
PAT3040_02336	CBM34(8-125),GH13(160-471)
PAT3040_02342	GH2(397-1012)
PAT3040_02348	GH38(4-263)
PAT3040_02349	GH2(21-707)
PAT3040_02371	GH117(79-205),GH117(208-321)
PAT3040_02381	GH63(226-528)
PAT3040_02383	GH109(2-103)
PAT3040_02384	GH109(22-137)
PAT3040_02391	GH28(28-354)
PAT3040_02424	GH109(15-126)
PAT3040_02425	CBM16(44-146)
PAT3040_02431	GH2(42-662)
PAT3040_02434	CBM40(41-88)
PAT3040_02457	CE1(24-240)
PAT3040_02495	CE4(413-571)

PAT3040_02502	CE3(55-205)
PAT3040_02535	GH109(7-126)
PAT3040_02539	CE3(82-209)
PAT3040_02543	GH141(24-545),CBM66(817-977),CBM66(1076-1222)
PAT3040_02559	GT4(193-334)
PAT3040_02565	GT4(226-373)
PAT3040_02576	GT26(60-228)
PAT3040_02585	GT2(3-158)
PAT3040_02586	GT2(8-161)
PAT3040_02624	GH141(110-292)
PAT3040_02639	GH130(16-330)
PAT3040_02648	CBM66(1416-1532)
PAT3040_02698	CE1(39-158)
PAT3040_02708	GT2(6-140)
PAT3040_02710	GT2(17-213)
PAT3040_02738	CBM50(273-313)
PAT3040_02787	GH109(7-122)
PAT3040_02789	GH109(5-115)
PAT3040_02797	PL8(617-874),CBM66(1041-1183),CBM66(1228-1354)
PAT3040_02843	AA2(60-174),AA2(449-706)
PAT3040_02854	GH42(14-389)
PAT3040_02856	GH140(10-437)
PAT3040_02864	GH78(58-578)
PAT3040_02866	GH2(43-933)
PAT3040_02906	GH95(1-339)
PAT3040_02910	GH105(32-360)
PAT3040_02913	GH109(6-114)
PAT3040_02916	CE9(9-346)
PAT3040_02923	CE1(51-275)
PAT3040_02926	AA3(25-313)
PAT3040_02940	CBM40(159-245)

PAT3040_02943	GH140(107-367)
PAT3040_02946	GH43(41-232)
PAT3040_02951	GH33(32-333)
PAT3040_02953	GH142(216-703)
PAT3040_02961	GH109(7-113)
PAT3040_02962	PL17(819-931)
PAT3040_02963	GH109(2-110)
PAT3040_02965	CE12(13-178)
PAT3040_02969	GH2(35-650)
PAT3040_02988	GH88(45-363)
PAT3040_02990	GH29(34-378)
PAT3040_03055	GH109(2-112)
PAT3040_03056	GH109(15-117)
PAT3040_03060	GH105(26-334)
PAT3040_03061	GH42(14-389)
PAT3040_03064	GH2(2-534)
PAT3040_03069	CE12(96-304),CE12(773-968)
PAT3040_03078	GH35(11-323)
PAT3040_03080	GH78(168-638)
PAT3040_03093	CBM32(47-181),CBM32(741-872),CBM32(1258-1397),CBM66(1441-1576),CBM66(2098-2251)
PAT3040_03099	CBM16(582-698),CBM16(1456-1575),CBM16(1612-1726),CBM54(222-332),CBM9(1279-1417)
PAT3040_03109	CE12(51-161)
PAT3040_03113	GH129(344-745)
PAT3040_03142	PL17(612-709)
PAT3040_03143	PL12(771-846)
PAT3040_03144	CE15(201-338),CE7(141-244)
PAT3040_03145	GH95(49-871)
PAT3040_03147	GH43(7-264)
PAT3040_03148	GH43(22-295)
PAT3040_03149	GH146(40-511)
PAT3040_03150	CBM37(886-944),CBM40(735-862),CBM40(1070-1171),CBM40(1258-1379)

PAT3040_03156	GH28(202-456)
PAT3040_03188	GH3(104-329)
PAT3040_03194	GH130(4-332)
PAT3040_03195	CBM56(150-238),CBM56(685-871),GH16(427-679)
PAT3040_03202	GH16(8-242)
PAT3040_03204	CE14(4-109)
PAT3040_03209	GH29(29-212)
PAT3040_03210	GH109(30-158)
PAT3040_03211	GH109(4-119)
PAT3040_03225	GH109(4-111)
PAT3040_03227	CE14(4-113)
PAT3040_03239	CBM67(124-305),GH78(331-847)
PAT3040_03260	CE4(34-141)
PAT3040_03282	GH43(8-274)
PAT3040_03300	GH130(21-335)
PAT3040_03306	CE3(62-200)
PAT3040_03329	CBM50(4-48),CBM50(65-109)
PAT3040_03357	CBM50(495-536)
PAT3040_03400	GH38(7-273)
PAT3040_03404	GH125(35-430)
PAT3040_03413	CE9(12-387)
PAT3040_03424	CBM16(667-769),GH16(43-294),GH16(327-586)
PAT3040_03445	CE1(2-180)
PAT3040_03477	CBM9(243-432)
PAT3040_03524	GH109(8-109)
PAT3040_03530	CE3(54-155)
PAT3040_03538	GH36(24-728)
PAT3040_03541	GH4(13-193)
PAT3040_03542	CBM32(538-653),CBM35(898-956)
PAT3040_03543	CBM16(921-979),CBM32(392-540),CBM32(767-884),CBM37(669-720)
PAT3040_03549	GH117(41-278)

PAT3040_03551	GH31(176-613)
PAT3040_03563	PL12(403-536)
PAT3040_03571	GH29(11-314)
PAT3040_03576	GH141(55-542),CBM32(743-855),CBM32(895-1007),CBM32(1039-1141),CBM32(1170-1283),CBM32(1562-1663),CBM46(1702-1771)
PAT3040_03577	GH109(1-110)
PAT3040_03583	GH109(30-121)
PAT3040_03601	AA3(157-704)
PAT3040_03631	GT4(168-316)
PAT3040_03632	GT2(2-125)
PAT3040_03633	GT4(187-291)
PAT3040_03634	GT2(11-116)
PAT3040_03636	GT32(26-104)
PAT3040_03652	GH106(1-672)
PAT3040_03660	GH76(53-209)
PAT3040_03664	GH31(324-578)
PAT3040_03667	CBM22(324-438)
PAT3040_03671	CE10(24-272)
PAT3040_03690	CBM67(12-198),GH78(478-984)
PAT3040_03698	GH78(469-746)
PAT3040_03725	AA6(28-103)
PAT3040_03747	PL8(404-681)
PAT3040_03750	GH5(67-390)
PAT3040_03758	CBM32(97-211),CBM32(229-342),CBM32(359-477),CBM32(839-957),CBM32(971-1086),CBM32(1102-1218)
PAT3040_03786	GH31(238-667)
PAT3040_03841	GH95(1-572)
PAT3040_03842	GH136(170-644)
PAT3040_03877	GH109(25-128)
PAT3040_03880	GH109(5-120)
PAT3040_03882	GH43(47-327),CBM66(373-483)
PAT3040_03886	GT2(9-124),GT21(77-197)
PAT3040_03902	GH88(43-364)

PAT3040_03926	GH29(9-343)
PAT3040_03946	GH73(25-150)
PAT3040_03963	CBM32(70-186),CBM32(229-342),CBM32(385-504)
PAT3040_03974	CE4(49-174)
PAT3040_04009	GH38(8-279)
PAT3040_04013	CBM32(561-654)
PAT3040_04014	CBM32(569-623),CBM32(690-758)
PAT3040_04016	GH109(32-111)
PAT3040_04062	GH109(5-112)
PAT3040_04074	GH78(200-695)
PAT3040_04079	GH109(2-117)
PAT3040_04080	CE12(139-308)
PAT3040_04083	CE7(42-281)
PAT3040_04090	GH129(91-749)
PAT3040_04094	CBM35(95-131)
PAT3040_04096	CE6(122-215)
PAT3040_04305	CE4(142-267)
PAT3040_04349	GH8(59-368)
PAT3040_04360	GH2(16-530)
PAT3040_04368	CBM32(50-171),CBM32(182-303),CBM32(325-443),CBM32(458-576),CBM32(1161-1212)
PAT3040_04382	GH26(217-362)
PAT3040_04414	GH109(3-120)
PAT3040_04437	CE4(5-128)
PAT3040_04456	GH109(4-117)
PAT3040_04468	CBM67(2-134),GH78(181-694)
PAT3040_04486	GH95(4-732)
PAT3040_04492	GH109(5-113)
PAT3040_04494	GH42(15-393)
PAT3040_04511	CE1(32-237)
PAT3040_04542	CBM32(191-326)
PAT3040_04557	CE1(48-285)

PAT3040_04579	GT28(209-340)
PAT3040_04620	GH109(4-119)
PAT3040_04622	CBM50(32-75)
PAT3040_04623	CE4(21-141)
PAT3040_04674	CBM16(55-151),CBM16(848-938),CBM9(404-555),GH42(1001-1288)
PAT3040_04677	GH105(28-339)
PAT3040_04687	GH38(3-252)
PAT3040_04693	CBM32(71-186)
PAT3040_04711	GH109(8-117)
PAT3040_04719	GH136(572-1076)
PAT3040_04727	CBM57(1116-1268)
PAT3040_04728	GH109(4-103)
PAT3040_04730	GH38(3-263)
PAT3040_04731	GH38(12-269)
PAT3040_04750	CE3(7-208)
PAT3040_04763	GH105(27-344)
PAT3040_04765	CE1(4-151)
PAT3040_04819	CE1(107-322)
PAT3040_04837	CE4(261-388)
PAT3040_04850	CBM16(55-144),CBM9(300-472),GH42(921-1203)
PAT3040_04856	GH4(7-184)
PAT3040_04879	CBM50(4-47),CBM50(55-98),GH18(176-407)
PAT3040_04899	CBM67(9-192),GH78(253-758)
PAT3040_04901	CE3(1155-1308)
PAT3040_04902	CE7(467-627)
PAT3040_04905	CE4(158-276)
PAT3040_04910	CE7(89-250)
PAT3040_04971	GH13(63-366),CBM26(637-700),CBM32(1446-1557)
PAT3040_05000	GH109(6-120)
PAT3040_05002	GH29(27-230)
PAT3040_05003	GH141(27-548),CBM32(650-757)

PAT3040_05050	GH2(2-735)
PAT3040_05054	CE3(58-212)
PAT3040_05056	CBM54(224-319),CBM16(425-508),GH5(734-822),CBM16(1345-1469)
PAT3040_05061	GH109(9-120)
PAT3040_05062	CE7(85-247),CE15(201-354)
PAT3040_05063	GH109(5-119)
PAT3040_05065	CE9(14-375)
PAT3040_05067	CBM16(766-892)
PAT3040_05069	GH42(20-390)
PAT3040_05070	PL12(412-550)
PAT3040_05088	GH4(3-180)
PAT3040_05107	CE12(141-305)
PAT3040_05111	CE1(123-347)
PAT3040_05121	GT2(3-138)
PAT3040_05139	CE12(6-205)
PAT3040_05144	PL11(44-648)
PAT3040_05146	PL26(9-858)
PAT3040_05155	PL21(325-391)
PAT3040_05181	CE7(4-316)
PAT3040_05182	GH43(43-337)
PAT3040_05183	GH43(9-301)
PAT3040_05188	**GH66(42-428,540-735),CBM35(42-541),CBM35(747-866)**
PAT3040_05194	GH109(6-113)
PAT3040_05195	**CBM35(6-99),CBM35(109-231),CBM61(244-392)**
PAT3040_05196	**putative GH31(238-667)**
PAT3040_05198	GH109(2-114)
PAT3040_05205	GH95(314-754)
PAT3040_05211	GH95(4-750)
PAT3040_05212	CE15(7-371)
PAT3040_05214	GH18(269-531)
PAT3040_05223	GH27(45-218),CBM46(516-583),CBM46(614-679),CBM46(842-895),CBM46(918-989),CBM46(1010-1082),CBM46(1338-1290)

PAT3040_05224	GH110(7-556)
PAT3040_05264	CBM32(64-122)
PAT3040_05273	CBM16(212-333),CBM70(39-191)
PAT3040_05280	GH105(29-366)
PAT3040_05287	GH43(14-295)
PAT3040_05288	GH127(19-448)
PAT3040_05323	GH13(73-426)
PAT3040_05330	GH2(110-819)
PAT3040_05352	GH9(409-853)
PAT3040_05356	PL12(403-494)
PAT3040_05404	CE1(20-151)
PAT3040_05405	CBM48(143-232),GH13(305-648)
PAT3040_05407	GH109(1-116)
PAT3040_05439	GH2(3-477)
PAT3040_05441	GH42(8-378)
PAT3040_05499	AA3(5-566)
PAT3040_05520	GH109(4-110)
PAT3040_05528	GH130(6-346)
PAT3040_05548	GH76(65-355),CBM35(388-509)
PAT3040_05550	GH76(34-326)
PAT3040_05570	GH130(6-345)
PAT3040_05601	GH109(3-114)
PAT3040_05655	GH26(142-268)
PAT3040_05659	GH109(4-99)
PAT3040_05674	CE9(4-383)
PAT3040_05699	GH109(6-119)
PAT3040_05757	GH109(5-116)
PAT3040_05761	CE15(24-325)
PAT3040_05774	CBM16(632-729),CBM6(715-841)
PAT3040_05788	GH29(18-316)
PAT3040_05811	GH109(4-115)

PAT3040_05812	GH109(3-108)
PAT3040_05814	GH38(2-215)
PAT3040_05821	GH109(4-118)
PAT3040_05849	CE7(29-335)
PAT3040_05866	CE1(6-237),CE1(312-520)
PAT3040_05888	GH116(386-742)
PAT3040_05889	CBM70(300-350)
PAT3040_05906	GH2(16-578)
PAT3040_05907	GH51(207-662)
PAT3040_05932	GH109(31-93),CBM9(351-511)
PAT3040_05933	GH20(66-281)
PAT3040_05976	GH109(5-121)
PAT3040_05979	GH143(497-668)
PAT3040_05983	CBM16(815-885),CBM16(916-1040)
PAT3040_06006	CE1(14-266)
PAT3040_06008	GH88(62-377)
PAT3040_06018	GH105(391-715)
PAT3040_06024	GH109(4-118)
PAT3040_06027	GH109(3-104)
PAT3040_06031	GH31(192-628)
PAT3040_06032	GH109(50-111)
PAT3040_06037	PL6(24-140)
PAT3040_06038	GH88(46-367)
PAT3040_06043	PL6(8-238)
PAT3040_06052	GH51(2-507)
PAT3040_06083	GH16(32-226)
PAT3040_06084	GH42(185-302)
PAT3040_06090	GH42(188-311)
PAT3040_06093	GH42(458-592)
PAT3040_06102	GH2(48-1017)
PAT3040_06110	GT51(81-256)

PAT3040_06138	CBM50(182-230)
PAT3040_06156	GH94(106-1097)
PAT3040_06191	CE4(81-204)
PAT3040_06226	GH109(4-121)
PAT3040_06232	GT2(8-166)
PAT3040_06264	GH3(64-286)
PAT3040_06277	CBM67(38-196),GH78(226-737)
PAT3040_06291	CE3(135-202)
PAT3040_06301	GH42(19-391)
PAT3040_06302	CBM32(445-516)
PAT3040_06308	CE14(3-118)
PAT3040_06383	GT28(211-362)
PAT3040_06391	CBM67(15-176),GH78(211-691)
PAT3040_06394	CBM16(114-223),GH39(425-714),CBM9(883-1078)
PAT3040_06437	CBM66(322-466),GH32(6-286)
PAT3040_06439	GH31(176-604)
PAT3040_06444	CE7(4-316)
PAT3040_06448	CBM51(997-1077)
PAT3040_06451	GH109(5-119)
PAT3040_06453	GT4(197-353)
PAT3040_06466	CE1(11-194)
PAT3040_06478	GH18(327-560)
PAT3040_06487	GH109(2-133)
PAT3040_06489	CBM9(34-214)
PAT3040_06501	CBM54(196-300)
PAT3040_06502	GH2(29-692)
PAT3040_06516	CBM22(39-171),CBM22(209-334),GH10(369-694),CBM9(721-893)
PAT3040_06545	GH42(15-131)
PAT3040_06562	GH2(8-739)
PAT3040_06569	GH42(20-390)
PAT3040_06575	GH106(11-728)

PAT3040_06580	GH95(2-393)
PAT3040_06582	GH105(34-375)
PAT3040_06583	PL22(34-274)
PAT3040_06586	GH105(4-140)
PAT3040_06596	GH109(2-116)
PAT3040_06598	GH106(7-817)
PAT3040_06616	CBM22(49-176),CBM22(235-354),CBM22(397-519)
PAT3040_06619	CBM61(38-158),CBM16(171-305),GH53(374-733),CBM32(1812-1923)
PAT3040_06620	GH115(28-462)
PAT3040_06625	CE6(87-166)
PAT3040_06669	GH38(232-491)
PAT3040_06703	CBM9(115-275),CBM16(553-653),GH42(708-982)
PAT3040_06705	GH78(302-568)
PAT3040_06722	AA6(3-93)
PAT3040_06746	GH43(27-322),CBM66(358-486)
PAT3040_06781	GH18(308-594)
PAT3040_06795	GT2(5-128)
PAT3040_06796	GT94(24-316)
PAT3040_06798	GT4(179-333)
PAT3040_06799	GT4(273-350)
PAT3040_06801	GT4(185-319)
PAT3040_06820	CBM50(4-46),CBM50(53-96)
PAT3040_06858	GT4(197-344)
PAT3040_06859	CE14(2-50)
PAT3040_06925	CE4(91-214)
PAT3040_07024	GH15(277-640)
PAT3040_07025	GT5(2-471)
PAT3040_07028	CBM48(29-112),GH13(180-487)
PAT3040_07030	CE10(277-442)
PAT3040_07151	GT2(86-283),GT21(252-336)
PAT3040_07152	GT2(12-141)

PAT3040_07199	GH4(3-180)
PAT3040_07201	GH51(3-497)
PAT3040_07202	CE1(12-255)
PAT3040_07209	GH109(29-117)
PAT3040_07213	GH3(150-372)
PAT3040_07225	GH141(4-523)
PAT3040_07245	GH43(6-316)
PAT3040_07248	AA6(23-102)
PAT3040_07257	AA7(20-179)
PAT3040_07258	GH39(110-483),CBM61(717-857)
PAT3040_07265	GH137(14-333)
PAT3040_07275	CE10(34-260)
PAT3040_07282	GH94(2-668)

GH, glycoside hydrolase family; GT, glycosyltransferase family; PL, polysaccharide lyase family; CE, carbohydrate esterase family; AA, auxiliary activities family; CBM, carbohydrate-binding module family

The genes of CITase (*cit*, PAT3040_05188) and a putative 6-α-glucosyltransferase (*6gt31a*, PAT3040_05195-05196) are shown in red color.

Dataset S1. Metabolome analysis of *P. agaridevorans* wild-type (T-3040) and triple mutant (YT478) strains[a]

Metabolite	Concentration (pmol/OD unit) 12 h		Comparative analysis		Concentration (pmol/OD unit) 48 h		Comparative analysis	
	Wild-type	Mutant (YT478)	Ratio	p-value	Wild-type	Mutant (YT478)	Ratio	p-value
Glyoxylic acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Glycolic acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Pyruvic acid	N.D.	N.D.	N.A.	N.A.	1685±374	N.D.	<1	N.A.
Lactic acid	3703±143	3837±686	1	0.771	728±390	250±9.3	0.3	0.167
2-Hydroxybutyric acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
3-Hydroxybutyric acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Fumaric acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
2-Oxoisovaleric acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Succinic acid	948±162	599±76	0.6	0.047	436±29	241±34	0.6	0.002
Malic acid	146±10	139±17	1	0.576	113±6.6	166±15	1.5	0.014
2-Oxoglutaric acid	N.D.	259	1<	N.A.	373±17	349	0.9	N.A.
Phosphoenolpyruvic acid	133±59	446±77	3.4	0.006	52±4.4	62±10	1.2	0.261
Dihydroxyacetone phosphate	41	134±22	3.3	N.A.	25±0.7	N.D.	<1	N.A.
Glyceraldehyde 3-phosphate	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Glycerol 3-phosphate	111±30	184±57	1.7	0.141	22±1.3	22±3.2	1	0.883
cis-Aconitic acid	N.D.	N.D.	N.A.	N.A.	43	N.D.	<1	N.A.
3-Phosphoglyceric acid	465±226	1565±406	3.4	0.024	2772±823	639±119	0.2	0.044
2-Phosphoglyceric acid	68±42	157±24	2.3	0.046	N.D.	N.D.	N.A.	N.A.
Citric acid	342±78	466±163	1.4	0.324	3550±536	138±39	0.04	0.008
Isocitric acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Gluconic acid	26	22	0.8	N.A.	184±79	N.D.	<1	N.A.
Erythrose 4-phosphate	67±36	113±21	1.7	0.281	N.D.	N.D.	N.A.	N.A.
Ribulose 5-phosphate	57±12	64±21	1.1	0.664	385±55	59±6.2	0.2	0.009
Ribose 5-phosphate	88±37	78±35	0.9	0.768	127±18	N.D.	<1	N.A.
Glucose 6-phosphate	207±167	527±229	2.5	0.129	71±24	25±1.1	0.3	0.079
Fructose 6-phosphate	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Glucose 1-phosphate	N.D.	32±2.5	1<	N.A.	N.D.	N.D.	N.A.	N.A.
6-Phosphogluconic acid	63±25	52±15	0.8	0.643	49±14	N.D.	<1	N.A.
Sedoheptulose 7-phosphate	79±25	72±4.7	0.9	0.709	1189±237	45±9.5	0.04	0.014
Fructose 1,6-diphosphate	185±147	1000±572	5.4	0.125	273±27	63±5.9	0.2	0.004
S-Adenosylmethionine	134±11	274±19	2	0.001	160±11	124±5.9	0.8	0.017
dTMP	19±1.5	30±4.7	1.6	0.046	36±9.3	11	0.3	N.A.
CMP	172±29	182±31	1.1	0.704	232±56	70±6.1	0.3	0.037
UMP	270±91	408±49	1.5	0.102	147±50	87±16	0.6	0.165
AMP	125±33	105±7.1	0.8	0.402	230±64	149±21	0.6	0.151
GMP	22±4.0	18±4.1	0.8	0.311	121±54	29±4.5	0.2	0.095
IMP	46±4.6	23±6.8	0.5	0.071	N.D.	N.D.	N.A.	N.A.
cAMP	N.D.	N.D.	N.A.	N.A.	19±1.2	N.D.	<1	N.A.
cGMP	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Cytosine	3.9±0.4	2.6±0.5	0.7	0.024	2.9±1.0	1.6	0.6	N.A.
Uracil	63±11	99±31	1.6	0.173	79±7.0	66±10	0.8	0.154
Thymine	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Adenine	73±12	126±18	1.7	0.017	21±1.4	5.8±0.4	0.3	0.002
Hypoxanthine	9.4±2.5	8.3	0.9	N.A.	94±3.4	16±1.4	0.2	1.00E-04
Guanine	41±11	47±4.6	1.2	0.412	14±2.3	12±0.8	0.8	0.177
Thymidine	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Cytidine	10±0.2	7.8±1.2	0.8	0.07	1.2±0.3	2.2±0.6	1.9	0.073
Uridine	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Adenosine	316±4.5	215±29	0.7	0.024	60±13	29±7.9	0.5	0.031
Guanosine	29±1.0	19±2.0	0.6	0.004	58±8.0	15±2.5	0.3	0.007
Inosine	N.D.	N.D.	N.A.	N.A.	95±5.4	N.D.	<1	N.A.
CoA_divalent	24±7.1	16	0.7	N.A.	N.D.	N.D.	N.A.	N.A.
PRPP	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
CDP	98±15	215±16	2.2	7.30E-04	266±43	120±24	0.4	0.013
UDP	731±65	1294±37	1.8	7.60E-04	174±10	97±9.7	0.6	7.20E-04
ADP	548±113	533±37	1	0.849	222±30	254±22	1.1	0.22
GDP	90±11	97±18	1.1	0.603	69±1.7	N.D.	<1	N.A.
dCTP	53±6.1	86±22	1.6	0.116	N.D.	N.D.	N.A.	N.A.
dTDP	74±10	139±25	1.9	0.033	38±4.3	N.D.	<1	N.A.
dTTP	57±3.4	56±9.7	1	0.833	N.D.	N.D.	N.A.	N.A.
dATP	N.D.	N.D.	N.A.	N.A.	16±1.2	N.D.	<1	N.A.
CTP	234	756±71	3.2	0.006	575±110	115±30	0.2	0.013
UTP	247±9.7	457±115	1.8	0.086	53±4.7	N.D.	<1	N.A.
ATP	970±45	1431±330	1.5	0.134	192±35	132±25	0.7	0.082
GTP	159±45	304±158	1.9	0.248	54±13	N.D.	<1	N.A.
Acetyl CoA_divalent	13	24±9.6	1.8	N.A.	27±2.1	10±2.2	0.4	0.01
Malonyl CoA_divalent	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
NAD$^+$	1448±285	978±12	0.7	0.104	404±42	847±74	2.1	0.002
NADP$^+$	146±60	147±13	1	0.972	182±26	145±8.0	0.8	0.121
Gly	2792±25	1983±202	0.7	0.019	1951±96	938±163	0.5	0.002
Ala	6998±239	5195±500	0.7	0.013	6156±350	2029±392	0.3	1.80E-04
Sarcosine	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
β-Ala	8.7±1.6	9±0.5	1	0.765	6.5±0.6	8.8±2.7	1.4	0.27
N,N-Dimethylglycine	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
GABA	72±1.1	52±7.3	0.7	0.037	50±3.8	19±2.7	0.4	5.90E-04
Choline	106±0.8	80±5	0.8	0.011	137±16	53±6.5	0.4	0.006
Ser	3675±88	2898±324	0.8	0.045	2736±133	1459±219	0.5	0.002
Creatinine	3.3±0.4	2.6±0.3	0.8	0.088	1.3±0.12	1.0±0.2	0.7	0.172
Pro	1638±94	3010±711	1.8	0.077	1456±48	701±136	0.5	0.006
Val	5138±85	4,534	0.9	0.073	3811±184	1933±365	0.5	0.004
Betaine	20308±1621	15575±4362	0.8	0.193	13957±1675	8192±1022	0.6	0.012
Homoserine	28±1.6	20±0.9	0.7	0.003	11±0.2	7.1±1.7	0.7	0.058
Thr	2861±72	2255±229	0.8	0.035	2591±60	1181±248	0.5	0.007
Betaine aldehyde_+H$_2$O	N.D.	N.D.	N.A.	N.A.	2.3±0.3	N.D.	<1	N.A.
Cys	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Hydroxyproline	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Creatine	1.8±0.6	2.5±0.3	1.4	0.137	2.2±0.2	N.D.	<1	N.A.
Ile	3452±121	2645±289	0.8	0.027	2553±195	1108±184	0.4	7.40E-04
Leu	10181±314	7645±834	0.8	0.023	7608±292	3148±605	0.4	0.002
Asn	1727±50	1170±180	0.7	0.026	57±19	N.D.	<1	N.A.
Ornithine	281±56	116±10	0.4	0.033	185±1.5	54±6.2	0.3	4.10E-04
Asp	5257±1323	3297±515	0.6	0.11	3317±126	1439±284	0.4	0.003
Anthranilic acid	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Tyramine	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Gln	2146±571	4107±665	1.9	0.019	2371±275	142±32	0.06	0.005
Lys	13512±376	30761±1933	2.3	0.003	11399±170	9589±782	0.8	0.051
Glu	23164±1143	22971±1873	1	0.888	10555±281	13650±2414	1.3	0.155
Met	2229±9.1	1948±262	0.9	0.204	1527±86	648±137	0.4	0.002
His	1278±55	1690±151	1.3	0.03	1002±32	483±74	0.5	0.002
Phe	6139±164	4608±490	0.8	0.023	4117±224	1768±351	0.4	0.001
Arg	6122±101	8326±604	1.4	0.022	3065±135	3022±349	1	0.857
Citrulline	94±14	39±2.2	0.4	0.021	72±22	17±4.1	0.2	0.048
Tyr	727±20	720±64	1	0.869	671±46	260±53	0.4	5.70E-04
Trp	653±16	458±64	0.7	0.028	506±29	258±50	0.5	0.004
Putrescine	9.1±2.8	11±1.2	1.2	0.419	12±1.4	9.5±1.1	0.8	0.044
Spermine	467±73	711±166	1.5	0.111	321±2.8	312±17	1	0.443
Spermidine	17838±2041	20396±3105	1.1	0.308	9316±996	9136±193	1	0.786
Carnosine	N.D.	N.D.	N.A.	N.A.	N.D.	N.D.	N.A.	N.A.
Glutathione (GSSG)_divalent	10±1.3	6.1±0.4	0.6	0.031	6±0.4	2.1±0.7	0.4	0.002
Glutathione (GSH)	41±15	7.4	0.2	N.A.	N.D.	N.D.	N.A.	N.A.

[a]Strains were grown to mid-exponential (12 h) or stationary (48 h) growth phase in LB-Dex medium at 30°C and harvested by filtration with membrane filters. Intracellular metabolites were extracted and subjected to metabolome analysis, as described in Materials and Methods. All experiments were performed in triplicate, and the data were expressed as mean ±standard deviation. The blue color represents metabolites that showed more than 2-fold differences between the wild-type and mutant strains. *S*-adenosylmethionine, ATP, GTP, UTP, and CTP are shown in red color.